

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Shah, Purvi

(ii) TITLE OF THE INVENTION: HUMAN CORNICHON PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0401 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADNOT04
(B) CLONE: 1318847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
1 5 10 15
Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp

			20					25				30			
Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys	Asn	Thr	Leu
		35					40					45			
Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala	Phe	Phe	Cys	Val
	50					55					60				
Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu	Gly	Leu	Asn	Met	Pro
65					70					75					80
Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met	Ser	Arg	Pro	Val	Met	Ser
				85					90					95	
Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr	Ile	Met	Asn	Ala	Asp	Ile	Leu
			100					105					110		
Ala	Tyr	Cys	Gln	Lys	Glu	Gly	Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu
		115					120					125			
Ala	Phe	Phe	Tyr	Tyr	Leu	Tyr	Gly	Met	Ile	Tyr	Val	Leu	Val	Ser	Ser
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT04
(B) CLONE: 1318847

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2;

GTTTTACCCA	GAGGGCCCTG	CGACGCCTTT	CTCGCTGGC	AACGGCGCCG	CTCCCCGCTC	60
CTCCTCCCCA	GCCATGGCGT	TCACGTTCGC	GGCCTTCTGC	TACATGCTGG	CGCTGCTGCT	120
CACTGCCGCG	CTCATCTTCT	TCGCCATTTG	GCACATTATA	GCATTTGATG	AGCTGAAGAC	180
TGATTACAAG	AATCCTATAG	ACCAGTGTAA	TACCCTGAAT	CCCCTTGTA	TCCCAGAGTA	240
CCTCATCCAC	GCTTCTTCT	GTGTCATGTT	TCTTTGTGCA	GCAGAGTGGC	TTACACTGGG	300
TCTCAATATG	CCCTTCTTGG	CATATCATAT	TGGAGGATAT	ATGAGTAGAC	CAGTGTATGAG	360
TGGCCCAGGA	CTCTATGACC	CTACAACCAT	CATGAATGCA	GATATTCTAG	CATATTGTCA	420
GAAGGAAGGA	TGGTGCAAAT	TAGCTTTTTA	TCTTCTAGCA	TTTTTTTACT	ACCTATATGG	480
CATGATCTAT	GTTTTGGTGA	GCTCTTAGAA	CAACACACAG	AAGAATTGGT	CCAGTTAAGT	540
GCATGCAAAA	AGCCACCAAA	TGAAGGGATT	CTATCCAGCA	AGATCCTGTC	CAAGAGTAGC	600
CTGTGGAATC	TGATCAGTTA	CTTTAAAAAA	TGACTCCTTA	TTTTTTTAAAT	GTTTCCACAT	660
TTTTGCTTGT	GGAAAGACTG	TTTTTCATATG	TTATACTCAG	ATAAAGATTT	TAAATGGTAT	720
TACGTATAAA	TTAATATAAA	ATGATTACCT	CTGGTGTTGA	CAGGTTTGAA	CTTGCACTTC	780
TTAAGGAACA	GCCATAATCC	TCTGAATGAT	GCATTAATTA	CTGACTGTCC	TAGTACATTG	840
GAAGCTTTTG	TTTATAGGAA	CTTGTAGGGC	TCATTTTGGT	TTCATTGAAA	CAGTATCTAA	900
TTATAAAATTA	GCTGTAGATA	TCAGGTGCTT	CTGATGAAGT	GAAAAATGTAT	ATCTGACTTAC	960
TGGGAAACCT	CATGGGTTTC	CTCATCTGTC	ATGTCGATGA	TTATATATGG	ATACATTTAC	1020
AAAAATAAAA	AGCGGGAATT	TTCCCTTCGC	TTGAATATTA	TCCCTGTATA	TGTCATGAAT	1080
GAGAGATTTC	CCATATTTC	ATCAGAGTAA	TAAATATACT	TGCTTTAATT	CTTAAGCATA	1140
AGTAAACATG	ATATAAAAAAT	ATATGCTGAA	TTACTTGTGA	AGAATGCATT	TAAAGCTATT	1200
TTAAATGTGT	TTTATTATTG	AAGACATTAC	TTATTAAGAA	ATTGGTTATT	ATGCTTACTG	1260
TTCTAATCTG	TGGTAAAGG	TATTCCTAAG	AATTTGCAGG	TACTACAGAT	TTTCAAAACT	1320
GAATGAGAGA	AAATTGTATA	ACCATTCTGC	TGTTCCCTTA	GTGCAATACA	ATAAACTCT	1380
GAAATTAAAA	A					1391

(2) INFORMATION FOR SEO ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
(B) CLONE: 886769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Phe	Asn	Phe	Thr	Ala	Phe	Thr	Tyr	Ile	Val	Ala	Leu	Ile	Gly
1				5					10					15	
Asp	Ala	Phe	Leu	Ile	Phe	Phe	Ala	Ile	Phe	His	Val	Ile	Ala	Phe	Asp
			20					25					30		
Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys	Asn	Ser	Leu
		35					40					45			
Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Leu	His	Ile	Phe	Leu	Asn	Leu
	50					55					60				
Leu	Phe	Leu	Phe	Cys	Gly	Glu	Trp	Phe	Ser	Leu	Cys	Ile	Asn	Ile	Pro
65					70				75					80	
Leu	Ile	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Lys	Asn	Arg	Pro	Val	Met	Ser
				85					90					95	
Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr	Val	Leu	Lys	Thr	Asp	Thr	Leu
			100					105					110		
Tyr	Arg	Asn	Met	Arg	Glu	Gly	Trp	Ile	Lys	Leu	Ala	Val	Tyr	Leu	Ile
		115					120					125			
Ser	Phe	Phe	Tyr	Tyr	Ile	Tyr	Gly	Met	Val	Tyr	Ser	Leu	Ile	Ser	Thr
	130						135				140				